Human 7TM Proteins and Polynucleotides Encoding the Same

In the claims:

Please amend claims 1 and 2, so that the text of the amended claims reads as follows.

1.(Amended) An isolated nucleic acid molecule containing [at least 24 contiguous bases of] the nucleotide sequence [first disclosed in the NGPCR nucleotide sequence] described in SEQ ID NO: 1.

2.(Amended) An isolated nucleic acid molecule comprising a nucleotide sequence that:

(a) encodes the amino acid sequence shown in SEQ ID NO: 2; and

(b) hybridizes under highly stringent conditions to the nucleotide sequence of SEQ ID NO: 1 or the complement thereof.

Please add new claim 7.

7.(New) A cell comprising the expression vector of Claim 6.

RESPONSE

I. Status of the Claims

Claims 3,4 and 5 have been canceled, as being drawn to a non-elected invention. Claims 1 and 2 have been amended. New claim 7 has been added. Claims 1, 2, 6 and 7 are therefore presently pending in the case. For the convenience of the Examiner, a clean copy of the pending claims is attached hereto as **Exhibit A**. In compliance with 37 C.F.R. § 1.121(c)(1)(ii), a marked up copy of the amended claims is attached hereto as **Exhibit B**.

II. Support for the Claims

Claim 1 has been amended to further clarify the claim, and to recite that the stringent hybridization conditions are highly stringent hybridization conditions. Support for this claim can be found throughout the specification as originally filed, with particular support being found at least in claim 1 and the sequence listing as originally filed.

Claim 2 has been amended to further clarify the claim, and to recite specifically stringent hybridization wash conditions. Support for this claim can be found throughout the specification as originally filed, with particular support being found at least in Claim 2 as originally filed and at page 7, lines 32-35.

New claim 7 has been added to more clearly claim aspects of the invention. Claim 7 finds support throughout the specification as originally filed, with particular support being found at page 14, lines 23-30.

As the amendments to Claim 1 and new Claim 7 are fully supported by the specification and claims as originally filed, they do not constitute new matter. Entry therefore is respectfully requested.

III. Objection

The Action objects to the use of the term "Novel" in the title of the application. Applicants have removed the offending term from the title of the application by amendment.

IV. Rejection of Claims Under 35 U.S.C. § 101

The Action rejects claims 1, 2 and 6 under 35 U.S.C. § 101, as allegedly lacking a patentable utility due to not being supported by a specific, substantial, and credible utility or, in the alternative, a well-established utility. Applicants respectfully traverse.

The present application describes a novel G-protein coupled receptor (GPCR). Of the pharmaceutical products currently being market by the entire industry, 60% of these drugs target G-protein coupled receptors (Gurrath, 2001, Curr. Med. Chem. *8*:1257-1299). Given that more than half of the currently marketed drugs target proteins that are structurally (7TM proteins) and functionally (G-protein interaction) related to the presently described sequences, a preponderance of the evidence clearly weighs in favor of Applicants' assertion that the presently described sequences have a specific (the claimed GPCR proteins are encoded by a specific locus on the human genome), credible, and well-established utility.

The Examiner states that "It is clear from the instant specification that the nucleic acid encoding the NGPCR polypeptide has been isolated because of its similarity to known proteins" (Action at page

4). The Examiner thent cites Doerks *et al.* (Trends in Genetics *14*:248-250, 1998) for the proposition that "sequence-to-function methods of assigning protein function are prone to errors" (Action at page 4). However, Doerks *et al.* states that "utilization of family information and thus a more detailed characterization" should lead to "simplification of update procedures for the entire families if functional information becomes available for at least one member" (Doerks *et al.*, page 248, paragraph bridging columns 1 and 2, emphasis added). The GPCR family is a well-studied protein family with a large amount of known functional information, exactly the situation that Doerks *et al.* suggests will "simplify" and "avoid the pitfalls" of previous sequence-to-function methods of assigning protein function (Doerks *et al.*, page 248, columns 1 and 2). Thus, instead of supporting the Examiner's position against utility, Doerks *et al.* actually supports Applicants' position that the presently claimed sequences have a substantial and credible utility.

The Examiner next cites Brenner (Trends in Genetics *15*:132-133, 1999) as teaching that "accurate inference of function form homology must be a difficult problem" (Action at page 4). However, this statement is based on the assumption that "if there are only 1000 superfamilies in nature, then most homologs must have different molecular and cellular functions" (page 132, second column). Furthermore, Brenner suggests that one of the main problems in using homology to predict function is "an issue solvable by appropriate use of modern and accurate sequence comparison procedures" (page 132, second column), and in fact references an article by Altschul *et al.*, which is the basis for one of the "modern and accurate sequence comparison procedures" used by Applicants. Thus, the Brenner article also does not support the alleged lack of utility.

The Examiner finally cites Bork *et al.* (Trends in Genetics *12*:425-427, 1996) as supporting the proposition that prediction of protein function from homology information by software robots (circa 1996) that assign functions to new proteins often assign a function based on the structural similarity of a small domain of the new protein to a small domain of a known protein (Action at page 4). Thus, the Examiner's reliance on Bork *et al.* has the same failing as described above for Doerks *et al.*, specifically, that the GPCR family is well studied and the assumption that Applicants assertion that the present sequences are GPCRs are made on the basis of structural similarity of a small domain of the new protein to a small domain of a known protein. Thus, Applicants assertion that the present sequences are GPCRs are not made on the basis of "structural similarity of a small domain of the new

protein to a small domain of a known protein", but rather homology over a large sequence. Thus, Bork *et al.* also does not support the alleged lack of utility for the present invention.

Rather, as set forth by the Federal Circuit, "(t)he threshold of utility is not high: An invention is 'useful' under section 101 if it is capable of providing some identifiable benefit." *Juicy Whip Inc. v. Orange Bang Inc.*, 51 USPQ2d 1700 (Fed. Cir. 1999) (citing *Brenner v. Manson*, 383 U.S. 519, 534 (1966)). Additionally, the Federal Circuit has stated that to violate § 101 the claimed invention "must be totally incapable of achieving a useful result." *Brooktree Corp. v. Advanced Micro Devices, Inc.*, 977 F.2d 1555, 1571 (Fed. Cir. 1992), emphasis added. *Cross v. Iizuka* (224 USPQ 739 (Fed. Cir. 1985)) states "any utility of the claimed compounds is sufficient to satisfy 35 U.S.C. § 101". *Id* at 748, emphasis added. Indeed, the Federal Circuit recently emphatically confirmed that "anything under the sun that is made by man" is patentable *(State Street Bank & Trust Co. v. Signature Financial Group Inc.*, 47 USPQ2d 1596, 1600 (Fed. Cir. 1998), citing the U.S. Supreme Court's decision in *Diamond vs. Chakrabarty*, 206 USPQ 193 (S.Ct. 1980)).

The Examiner accepts that the claimed sequence "is an orphan G-Protein coupled receptor" (Action at page 2), but states that this is not indicative of the claimed sequence having a specific, substantial and credible utility, because "further research" would be required to determine the usefulness of the protein (Action at page 5). However, this is incorrect as a matter of law. As the protein of the instant invention belongs to a family of compounds with a common, well established specific and substantial utility, the Federal Circuit's ruling in *In re Brana,* (34 USPQ2d 1436 (Fed. Cir. 1995), "*Brana*") is completely on point. In *Brana*, the Federal Circuit admonished the P.T.O. for confusing "the requirements under the law for obtaining a patent with the requirements for obtaining government approval to market a particular drug for human consumption". *Brana* at 1442. The Federal Circuit went on to state:

> At issue in this case is an important question of the legal constraints on patent office examination practice and policy. The question is, with regard to pharmaceutical inventions, what must the applicant provide regarding the practical utility or usefulness of the invention for which patent protection is sought. This is not a new issue; it is one which we would have thought had been settled by case law years ago.

Brana at 1439, emphasis added. The choice of the phrase "utility or usefulness" in the foregoing quotation is highly pertinent. The Federal Circuit is evidently using "utility" to refer to rejections under

35 U.S.C. § 101, and is using "usefulness" to refer to rejections under 35 U.S.C. § 112, first paragraph. This is made evident in the continuing text in *Brana*, which explains the correlation between 35 U.S.C. §§ 101 and 112, first paragraph. The Federal Circuit concluded:

> FDA approval, however, is not a prerequisite for finding a compound useful within the meaning of the patent laws. Usefulness in patent law, and in particular in the context of pharmaceutical inventions, necessarily includes the expectation of further research and development. The stage at which an invention in this field becomes useful is well before it is ready to be administered to humans. Were we to require Phase II testing in order to prove utility, the associated costs would prevent many companies from obtaining patent protection on promising new inventions, thereby eliminating an incentive to pursue, through research and development, potential cures in many crucial areas such as the treatment of cancer.

Brana at 1442-1443, citations omitted.

The Examiner seems to be requiring data that shows objective evidence that the "instant DNA or encoded protein" is associated with any "diseases or disorders" (Action at page 4). However, as stated above in *Brana*, the Federal Circuit has clearly stated that this is not the standard for utility under 35 U.S.C. § 101. The Examiner states that a "real-world" utility does not require further research (Action at page 5). However, even if, *arguendo*, further research might be required in certain aspects of the present invention, this does not preclude a finding that the invention has utility, as set forth by the Federal Circuit's holding in *Brana*, which clearly states, as highlighted in the quote above, that "pharmaceutical inventions, necessarily includes the expectation of further research and development" (*Brana* at 1442-1443, emphasis added). In assessing the question of whether undue experimentation would be required in order to practice the claimed invention, the key term is "undue", not "experimentation". *In re Angstadt and Griffin*, 190 USPQ 214 (CCPA 1976). The need for some experimentation does not render the claimed invention unpatentable. Indeed, a considerable amount of experimentation may be permissible if such experimentation is routinely practiced in the art. *In re Angstadt and Griffin, supra*; *Amgen, Inc. v. Chugai Pharmaceutical Co., Ltd.*, 18 USPQ2d 1016 (Fed. Cir. 1991). As a matter of law, it is well settled that a patent need not disclose what is well known in the art. *In re Wands*, 8 USPQ 2d 1400 (Fed. Cir. 1988).

As just one example of utility of the present nucleotide sequences, Applicants point out that, as taught in the specification as originally filed, at least at page 8, the claimed polynucleotide sequences can be used to track the expression of the genes encoding the described proteins. In particular, the

specification describes how the described sequences can be represented using a gene chip format to provide a high throughput analysis of the level of gene expression. Such "DNA chips" clearly have utility, as evidenced by hundreds of issued U.S. Patents, as exemplified by U.S. Patent Nos. 5,445,934, 5,556,752, 5,744,305, 5,837,832, 6,156,501 and 6,261,776. Evidence of the "real world" substantial utility of the present invention is provided by the fact that there is an entire industry established based on the use of gene sequences or fragments thereof in a gene chip format. Perhaps the most notable gene chip company is Affymetrix. However, there are many companies which have, at one time or another, concentrated on the use of gene sequences or fragments, in gene chip and non-gene chip formats, for example: Agilent Technologies, Gene Logic, ABI-Perkin-Elmer, HySeq and Incyte. In addition, one such company, Rosetta Inpharmatics, was viewed to have such "real world" value (net equity value of the transaction was $620 million) that it was acquired by large pharmaceutical company, Merck & Co., for significant sums of money. The "real world" substantial industrial utility of gene sequences or fragments would, therefore, appear to be widespread and well established. The sequences of the present invention describe a novel gene encoding a GPCR and provide a unique identifier of the corresponding gene. Such gene chips clearly have utility, as evidenced by hundreds of issued U.S. Patents, such as U.S. Patent Nos. 5,445,934, 5,556,752, 5,744,305, 5,837,832, 6,156,501 and 6,261,776. The present nucleotide sequences clearly encode human GPCRs, as detailed throughout the specification. The specification also teaches that GPCRs are associated with a wide variety of cellular functions, and as such, that GPCR interacting proteins have been subject to intense scrutiny as potential drug targets. Therefore, as the present sequences are specific markers of the human genome, and such specific markers are targets for the discovery of drugs that are associated with human disease, those of skill in the art would instantly recognize that the present nucleotide sequences would be an ideal, novel candidate for assessing gene expression using such gene chips. Clearly, compositions that enhance the utility of such DNA chips, such as the presently claimed nucleotide sequences, must in themselves be useful. Thus, the present claims clearly meet the requirements of 35 U.S.C. § 101.

Although Applicants need only make one credible assertion of utility to meet the requirements of 35 U.S.C. § 101 (*Raytheon v. Roper*, 220 USPQ 592 (Fed. Cir. 1983); *In re Gottlieb*, 140 USPQ 665 (CCPA 1964); *In re Malachowski*, 189 USPQ 432 (CCPA 1976); *Hoffman v. Klaus*,

9 USPQ2d 1657 (Bd. Pat. App. & Inter. 1988)), as a further example of the utility of the presently claimed polynucleotides, the Examiner is respectfully reminded that only a minor percentage of the genome actually encodes exons, which in-turn encode amino acid sequences. The presently claimed polynucleotide sequences provide biologically validated empirical data (*e.g.*, showing which sequences are transcribed, spliced, and polyadenylated) that *specifically* define that portion of the corresponding genomic locus that actually encodes exon sequence. Equally significant is that the claimed polynucleotide sequences define how the encoded exons are actually spliced together to produce an active transcript (*i.e.*, the described sequences are useful for functionally defining exon splice-junctions). The Applicants respectfully submit that the practical scientific value of expressed, spliced, and polyadenylated mRNA sequences is readily apparent to those skilled in the relevant biological and biochemical arts. For further evidence in support of the Applicants' position, the Examiner is requested to review, for example, section 3 of the Venter *et al.* article (Science, 2001, *291*:1304 *at* pp. 1317-1321, including Fig. 11 at pp.1324-1325), which demonstrates the significance of expressed sequence information in the structural analysis of genomic data. The presently claimed polynucleotide sequences define biologically validated sequences that provide a unique and specific resource for mapping genome essentially as described in the Venter *et al.* article Thus, the present claims clearly meet the requirements of 35 U.S.C. § 101.

Furthermore, persons of skill in the art, as well as thousands of venture capitalists and investors, readily recognize the utility, both scientific and commercial, of genomic data in general, and specifically human genomic data. Billions of dollars have been invested in the human genome project, resulting in useful genomic data (see, *e.g.*, Venter *et al.*, 2001, Science *291*:1304). The results have been a stunning success, as the utility of human genomic data has been widely recognized as a great gift to humanity (see, *e.g.*, Jasny and Kennedy, 2001, Science *291*:1153). Clearly, the usefulness of human genomic data, such as the presently claimed nucleic acid molecules, is substantial and credible (worthy of billions of dollars and the creation of numerous companies focused on such information) and well-established (the utility of human genomic information has been clearly understood for many years).

The legal test for utility simply involves an assessment of whether those skilled in the art would find any of the utilities described for the invention to be credible or believable. According to the Examination Guidelines for the Utility Requirement, if the applicant has asserted that the claimed

invention is useful for any particular purpose (i.e., it has a "specific and substantial utility") and the assertion would be considered credible by a person of ordinary skill in the art, the Examiner should not impose a rejection based on lack of utility (66 Federal Register 1098, January 5, 2001).

Additionally, methods similar to those of the present invention were used to identify the GPCR of issued U.S. Patent 6,043,052. Issued U.S. Patents are presumed to be valid and to meet the requirements of 35 U.S.C. §§ 101, 102, 103 and 112, specifically, that they have utility, are novel, non-obvious, are enabled, meet the written description requirements and particularly point out and distinctly claim the invention. Therefore, the Applicants' assertion that the described GPCR is in fact a GPCR is supported by issued U.S. Patent 6,043,052, as well as the plethora of other GPCR patents that the office has issued. For example, the specific and substantial utility of human GPCRs is evidenced by the fact that they are the subject of the above mentioned U.S. Patent No. 6,043,052 which discloses polynucleotides encoding a novel GPCR and U.S. Patent Nos. 5,891,646 and 6,110,693, both of which disclose and claim methods for detecting GPCR activity *in vivo* and *in vitro*, methods for assaying GPCR activity, and methods of screening for GPCR ligands, GPCR kinase activity, components that interact with GPCR regulatory processes and constructs useful in such methods. The issuance of these U.S. patents clearly indicates that GPCR polynucleotides have utility and that such utilities were sufficiently specific and substantial to warrant the issuance of U.S. patents directed to methods used to identify and characterize GPCRs. The teachings of these patentable disclosures are directly applicable to the present invention (GPCR polynucleotides) and are evidence that those skilled in the art recognize the specific and substantial utility of GPCRs. In light of the issuance of U.S. Patent No. 6,043,052 on polynucleotides encoding a novel GPCR, Applicants respectfully submit that the present application, which also describes polynucleotides encoding a novel GPCR, describes an invention with specific and substantial utility fully compliant with 35 U.S.C. § 101.

For each of the foregoing reasons, Applicants submit that the rejection of claims 1, 2 and 6 under 35 U.S.C. § 101 have been overcome, and request that the rejection be withdrawn.

V. Rejection of Claims Under 35 U.S.C. § 112, First Paragraph

The Action rejects claims 1, 2 and 6 under 35 U.S.C. § 112, first paragraph, since allegedly one skilled in the art would not know how to use the invention, as the invention allegedly is not supported by a specific, substantial, and credible utility or a well-established utility. Applicants respectfully traverse.

Applicants submit that claims 1, 2 and 6 have been shown to have "a specific, substantial, and credible utility", as detailed in section III above. Applicants therefore request that the rejection of claims 1, 2 and 6 under 35 U.S.C. § 112, first paragraph, be withdrawn.

VI. Rejection of Claims Under 35 U.S.C. § 112, First Paragraph

The Action next rejects Claim 1 under 35 U.S.C. § 112, first paragraph, as allegedly lacking enablement. Applicants respectfully traverse.

First, Applicants in no way agree with the Examiner's position that Claims 1, 2 and 6 lack enablement, as the claim as originally filed is fully operative. The Action states (on page 6) that the specification, while being enabling for a nucleic acid sequence of SEQ ID NO:1 does not reasonably enable a nucleic acid containing 24 contiguous bases of SEQ ID NO:1, or a nucleic acid which hybridizes to SEQ ID NO:1. However, solely in order to progress the case more rapidly to allowance, Applicants have amended Claim 1 to recite the full length molecule, which the Examiner admits is fully enabled.

With regard to Claim 2, Applicants submit that molecules which encode the amino acid sequence shown in SEQ ID NO: 2; and hybridize under stringent conditions to the nucleotide sequence of SEQ ID NO: 1 or the complement thereof, is a finite and well defined group, which those of skill in the art could easily identify and would know how to make and use.

VII. Rejection of Claims 1 and 2 Under 35 U.S.C. § 112, First Paragraph

35 U.S.C. § 112, first paragraph, requires that the specification contain a written description of the invention. The Federal Circuit in *Vas-Cath Inc. v. Mahurkar* (19 USPQ2d 1111 (Fed. Cir. 1991); "*Vas-Cath*") held that an "applicant must convey with reasonable clarity to those skilled in the art that, as of the filing date sought, he or she was in possession *of the invention*." *Vas-Cath*, at 1117,

emphasis in original. However, it is important to note that the above finding uses the terms reasonable clarity to those skilled in the art. Further, the Federal Circuit in *In re Gosteli* (10 USPQ2d 1614 (Fed. Cir. 1989); "*Gosteli*") held:

> Although [the applicant] does not have to describe exactly the subject matter claimed, . . . the description must clearly allow persons of ordinary skill in the art to recognize that [he or she] invented what is claimed.

Gosteli at 1618, emphasis added. Additionally, *Utter v. Hiraga* (6 USPQ2d 1709 (Fed. Cir. 1988); "*Utter*"), held "(a) specification may, within the meaning of 35 U.S.C. § 112 ¶1, contain a written description of a broadly claimed invention without describing all species that claim encompasses" (*Utter*, at 1714). Therefore, all Applicants must do to comply with 35 U.S.C. § 112, first paragraph, is to convey the invention with reasonable clarity to the skilled artisan.

Further, the Federal Circuit has held that an adequate description of a chemical genus "requires a precise definition, such as by structure, formula, chemical name or physical properties" sufficient to distinguish the genus from other materials. *Fiers v. Sugano*, 25 USPQ2d 1601, 1606 (Fed. Cir. 1993; "*Fiers*"). *Fiers* goes on to hold that the "application satisfies the written description requirement since it sets forth the . . . nucleotide sequence" (*Fiers* at 1607). In other words, provision of a structure and formula - the nucleotide sequence - renders the application in compliance with 35 U.S.C. § 112, first paragraph.

More recently, the standard for complying with the written description requirement in claims involving chemical materials has been explicitly set forth by the Federal Circuit:

> In claims involving chemical materials, generic formulae usually indicate with specificity what the generic claims encompass. One skilled in the art can distinguish such a formula from others and can identify many of the species that the claims encompass. Accordingly, such a formula is normally an adequate description of the claimed genus. *Univ. of California v. Eli Lilly and Co.*, 43 USPQ2d 1398, 1406 (Fed. Cir. 1997).

Thus, a claim describing a genus of nucleic acids by structure, formula, chemical name or physical properties sufficient to allow one of ordinary skill in the art to distinguish the genus from other materials meets the written description requirement of 35 U.S.C. § 112, first paragraph. As further elaborated by the Federal Circuit in *Univ. of California v. Eli Lilly and Co.*:

> In claims to genetic material ... a generic statement such as 'vertebrate insulin cDNA' or 'mammalian insulin cDNA', without more, is not an adequate written description of the genus because it does not distinguish the claimed genus from others, except by function. It does not specifically define any of the genes that fall within its definition. It does not define any structural features commonly possessed by members of the genus that distinguish them from others. One skilled in the art cannot, as one can do with a fully described genus, visualize or recognize the identity of members of the genus. (Emphasis added)

Thus, as opposed to the situation set forth in *Univ. of California v. Eli Lilly and Co.* and *Fiers*, the nucleic acid sequences of the present invention are not distinguished on the basis of function, or a method of isolation, but in fact are distinguished by structural features - a chemical formula, *i.e.*, the *sequence itself.*

Using the nucleic acid sequences of the present invention (as set forth in the Sequence Listing), the skilled artisan would readily be able to distinguish the claimed nucleic acids from other materials on the basis of the specific structural description provided. Polynucleotides comprising the nucleotide sequence of , for example, SEQ ID NO:1, or a nucleotide sequence that encodes SEQ ID NO:2, are within the genus of the instant claims, while those that lack this structural feature lie outside the genus. Claim 1 thus meets the written description requirement. Similarly, as defined in Claim 2, those of skill in the art would readily recognize isolated nucleic acid molecules having a nucleotide sequence that: (a) encodes the amino acid sequence shown in SEQ ID NO: 2; and (b) hybridizes under stringent conditions to the nucleotide sequence of SEQ ID NO: 1 or the complement thereof.

The Action, on page 9, lines 1-4, states that one skilled in the art cannot reasonably conclude the applicant had possession of the claimed invention at the time the instant application was filed. Applicants respectfully disagree. The skilled artisan would easily recognize 24 contiguous nucleic acids derived from any of the nucleic acid sequences described in the sequence listing and would also know

how to use a nucleic acid molecule that comprises 24 contiguous bases of nucleic acid sequence of SEQ ID NO:1. In fact, Applicants note that the entire DNA gene chip industry is based on the use of 24 or more contiguous bases of nucleic acid sequence. Therefore, Applicants submit that those of skill in the art would also be able to make and use the present invention.

However, having demonstrated that the present invention meets both the requirements for written description and enablement, for each of the foregoing reasons, Applicants submit that the rejection of Claims 1 and 2 under 35 U.S.C. § 112, first paragraph, has in part been avoided by amendment of Claim 1 to read on the full-length molecule and in part traversed and therefore respectfully request that the rejection be withdrawn.

VIII. Rejection of Claims 1 and 2 Under 35 U.S.C. § 112, Second Paragraph

The Action next rejects Claim 1 and 2 under 35 U.S.C. § 112, second paragraph, as allegedly being indefinite for failing to particularly point out and distinctly claim the invention. Specifically, the Action rejects Claim 1 as allegedly indefinite based on the recitation of the terms "NGPCR" and "first". While Applicants submit that the terms are sufficiently definite, NGPCR defined in the specification as novel GPCR, and "first" referring to the first disclosed, a term that would be known to those of skill in the art, solely in order to progress the case more rapidly toward allowance the claim has been revised to remove these terms. Applicants therefore submit that rejection of Claim 1 under 35 U.S.C. § 112, second paragraph, has been avoided and respectfully request withdrawal.

The Action also rejects Claim 2 under 35 U.S.C. § 112, second paragraph, as allegedly being indefinite for failing to particularly point out and distinctly claim the invention. Specifically, the Action rejects Claim 2 as allegedly indefinite based on the term "stringent hybridization conditions". While Applicants submit that the term is sufficiently definite, as a number of stringent hybridization conditions are defined in the specification and would be known to those of skill in the art, solely in order to progress the case more rapidly toward allowance the claim has been revised to recite "highly stringent hybridization conditions". As the specification provides specific teaching regarding "highly stringent hybridization conditions", at least at page7, lines 32-35, Applicants submit that revised Claim 2 even more clearly meets the requirements of 35 U.S.C. § 112, second paragraph. Applicants stress that "a claim need not 'describe' the invention, such description being the role of the disclosure".

Orthokinetics, Inc. v. Safety Travel Chairs, Inc., 1 USPQ2d 1081, 1088 (Fed. Cir. 1986). Based on the foregoing, Applicants submit that Claim 2 is sufficiently definite, and respectfully request withdrawal of this rejection.

IX. Rejection of Claims Under 35 U.S.C. § 102(b)

The Action next rejects claims 1 and 2 under 35 U.S.C. § 102(b), as being anticipated by an EST described by Hillier *et al.* (1996, accession no. T71087). While Applicants do not necessarily agree with the present rejection, as claim 1 has been amended to recite the complete nucleotide sequence of SEQ ID NO: 1, which is neither taught nor suggested by the EST of Hillier *et al.* (1996), applicants respectfully request withdrawal of the rejection of Claim 1 under 35 U.S.C. § 102(b).

Applicants respectfully submit that rejection of Claim 2 under under 35 U.S.C. § 102(b), as being anticipated by Hillier *et al.* (1996, accession no. T71087), is in error because while the EST nucleic acid sequence of Hillier *et al.* (1996) might hybridize to a molecule comprising the nucleic acid sequence SEQ ID NO: 1, it would not encode, nor suggest the entire amino acid sequence of SEQ ID NO:2. Therefore, Applicants submit that the rejection of claims 1 and 2 under 35 U.S.C. § 102(b) have been avoided, and respectfully request withdrawal of the rejection.

X. Conclusion

The present document is a full and complete response to the Action. In conclusion, Applicants submit that, in light of the foregoing remarks, the present case is in condition for allowance, and such favorable action is respectfully requested. Should Examiner Murphy have any questions or comments, or believe that certain amendments of the claims might serve to improve their clarity, a telephone call to the undersigned Applicants' representative is earnestly solicited.

Respectfully submitted,

October 1, 2002

Date

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Exhibit A

Clean Version of The Pending Claims in U.S. Patent Application Ser. No. 09/658,283

1.(Amended) An isolated nucleic acid molecule containing the nucleotide sequence described in SEQ ID NO: 1.

2.(Amended) An isolated nucleic acid molecule comprising a nucleotide sequence that:

(a) encodes the amino acid sequence shown in SEQ ID NO: 2; and

(b) hybridizes under highly stringent conditions to the nucleotide sequence of SEQ ID NO: 1 or the complement thereof.

6. An expression vector comprising an isolated polynucleotide encoding the amino acid sequence presented in SEQ ID NO: 2.

7.(New) A cell comprising the expression vector of Claim 6.